

## SEQUENCE LISTING

## Sequence Listing

<110> Nara Institute of Science, Technology, Research Institute of Innovative Technology  
for the Earth and Kinki University

<120> Transgenic plants

<130> C01F1576

<160> 17

<210> 1

<211> 358

<212> PRT

<213> *Spinacia oleracea* L

<220> Fructose-1, 6-bisphosphatase

<223>

<400> 1

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      20                      25                      30
Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser
      35                      40                      45
Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser
      50                      55                      60
Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln
      65                      70                      75                      80
Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg
      85                      90                      95
Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro
      100                     105                     110
Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp
      115                     120                     125
Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser
      130                     135                     140
Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp
      145                     150                     155                     160
His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val
      165                     170                     175
Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met
      180                     185                     190
Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr

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195	200	205
Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu		
210	225	220
Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly		
225	230	235
Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu		
245	250	255
Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly		
260	265	270
Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr		
275	280	285
Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu		
290	295	300
Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys		
305	310	315
Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile		
325	330	335
His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys		
340	345	350
Leu Glu Lys Tyr Leu Ala		
355		

&lt;210&gt; 2

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Fructose-1,6-bisphosphatase

&lt;223&gt;

&lt;400&gt; 2

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accatcggtt tttctagcat ttcatlggct tgltaacaaa ttgcttcctt gggtcaacga	180
gctggatatt ctaactlgac tggattcaa ggtgctgtca atatccaagg agaggatcag	240
aagaaacttg atgttgtctc caatgagggt ttttcgagct gcttgagatc gattggaaga	300
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cacgacgatg agtcacagct aagtgcagaa gaacagaggt gtgtagttaa tgtatgtcaa	540
ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgia	600
cttacaattg gtaaaaggtgt gtatgcattc acattagatc caatgtatgg tgaattcgta	660
ctcacttcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt	720

aactacaaaa tgigggaiga taaattgaag aaglacatgg atgatcttaa agagccagga 780  
 gaticacaga aaccgtactc gtcctgttac ataggagatt tagttgggga ctttcataga 840  
 acacttttat atgggtgggat ttaigtgttac ccaagagatg caaagagtaa gaatgggaaa 900  
 ttgaggcttt tgtatgaatg tgcacctatg agttttattg ttgaacaagc tgggtggtaaa 960  
 gggttcgatg gtcacaaag aattcttgac attcaaccca ccgagataca tcaacgtgtg 1020  
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<210> 3

<211> 333

<212> PRT

<213> Spinacia oleracea L

<220> Sedoheptulose-1,7-bisphosphatase

<223>

<400> 3

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 Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu  
                   20                  25                  30  
 Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe  
                   35                  40                  45  
 Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe  
                   50                  55                  60  
 Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe  
                   65                  70                  75                  80  
 Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu  
                   85                  90                  95  
 Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser  
                   100                  105                  110  
 Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe  
                   115                  120                  125  
 Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly  
                   130                  135                  140  
 Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro  
                   145                  150                  155                  160  
 Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
                   165                  170                  175  
 Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
                   180                  185                  190  
 Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
                   195                  200                  205  
 Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu

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210	215	220
Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln		
225	230	235
Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr		
245	250	255
Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe		
260	265	270
Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val		
275	280	285
Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr		
290	295	300
Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser		
305	310	315
Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala		
325	330	

&lt;210&gt; 4

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Spinacia oleracea L

&lt;220&gt; Sedoheptulose-1,7-bisphosphatase

&lt;223&gt;

&lt;400&gt; 4

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggigg aactcaatgt	180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc	240
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&lt;210&gt; 5

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&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus  
PCC 7942

&lt;223&gt;

&lt;400&gt; 5

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Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala
      20              25              30
Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu
      35              40              45
Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro
      50              55              60
Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys
      65              70              75              80
Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val
      85              90              95
Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser
      100             105             110
Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro
      115             120             125
Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys
      130             135             140
Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu
      145             150             155             160
Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg
      165             170             175
Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg
      180             185             190
Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly
      195             200             205
Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro
      210             215             220
Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe
      225             230             235             240
Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile
      245             250             255
Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile

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260 265 270  
 Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
 275 280 285  
 Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
 290 295 300  
 Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
 305 310 315 320  
 Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
 325 330 335  
 Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
 340 345 350  
 Arg Pro Glu Arg  
 355

&lt;210&gt; 6

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Synechococcus

<220> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from Synechococcus PCC. 7942

&lt;400&gt; 6

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&lt;210&gt; 7

&lt;211&gt; 133

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA promoter

&lt;400&gt; 7

agcttctaca tacaccttgg ttgacacgag tatataagtc atgttatact gttgaataac	60
aagccttcca ttttctatct tgattttagt aaaactagtg tgcttgggag tccctgatga	120
ttaataaac caa	133

&lt;210&gt; 8

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rps16 terminator

&lt;400&gt; 8

agcttgaat tcaattaaagg aaataaatta aggaaataca aaaagggggg tagtcatttg	60
tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct	120
atttgtatct ttttatcatt gcttccattg aattactag	159

&lt;210&gt; 9

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;223&gt; aadA

&lt;400&gt; 9

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gcgtcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtac ggctccgcag	120
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&lt;210&gt; 11

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; multi-cloning regions

&lt;400&gt; 11

ccaagatcta aaaggagaaa ttaagcatgc tctagatcga tgaattcgcc c 51

&lt;210&gt; 12

&lt;211&gt; 142

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; rrn promoter

&lt;400&gt; 12

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 ctggataca gttgtaggga gg 142

&lt;210&gt; 13

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;223&gt; psbA terminator

&lt;400&gt; 13

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 ctaicaagag ggtgctattg ctcttttctt tttttcttct tatttatcta ctagtatttt 120  
 acttacatag acttttttgt ttacattata gaaaaagaag gagaggttat tttcttgcac 180  
 ttattcatga ttgagtattc tattttgatt ttgtatttgt ttaaaattgt agaaatagaa 240  
 cttgtttctc ttcttgctaa tgttactata tctttttgat ttttttttcc caaaaaaaaa 300  
 tcaaattttg acttcttctt atctcttata ttgaataatc tcttatcttt gaaataataa 360  
 tatcatigaa ataagaaaga agagctatat 390

&lt;210&gt; 14

&lt;211&gt; 5581

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; pLD200

&lt;400&gt; 14

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c	5581

&lt;210&gt; 15

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; rbcL

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 705

&lt;212&gt; DNA

<213> *Nicotiana tabacum*

&lt;223&gt; accD

&lt;400&gt; 16

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 ttgiggtggt gaaagtcgaa atagtagtga aaacgagggt tccagtagac gaactcgcac 660  
 gaagggcagt gatttaacta taagagaaag ttctaataat ctcga 705

&lt;210&gt; 17

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; polylinker

&lt;400&gt; 17

cgcgcccgcg ctagcgtcga c 21

&lt;210&gt; 18

&lt;211&gt; 7

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;223&gt; Shine-Dalgarno Sequence

&lt;400&gt; 18

aggaggu

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